

/organism="Heterosigma akashiwo"
 /db_xref="taxon:2829"
 /note="isolated from red-tide sea water in Masan Bay,
 Korea; classified by morphological studies"
 <1..>712
 /note="variable domains D1 and D2"
 /product="24S large subunit ribosomal RNA"
 BASE COUNT 164 a 149 c 211 g 188 t
 ORIGIN Query Match 100.0%; Score 23; DB 8; Length 712;
 Best Local Similarity 100.0%; Pred. No. 0.15; Matches 23;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Features 3 (bases 1 to 715)
 REFERENCE Tyrrell,J.V., Bergquist,P.R., MacKenzie,L. and Bergquist,P.L.
 AUTHORS Phlogeny of the Raphidophytes Based on Large-Subunit rRNA Gene
 TITLE Sequences
 JOURNAL Unpublished
 JOURNAL Tyrrell,J.V., Bergquist,P.R., MacKenzie,L. and Bergquist,P.L.
 AUTHORS Direct Submission
 TITLE Submitted (02-DEC-1999) Research and Development, Monterey Bay
 JOURNAL Aquarium Research Institute, 7700 Sandholdt Road, Moss Landing, CA
 95039-0628, USA
 Query Match 1 ACCAGACTGACCAACCACTT 23
 Qy 1 ACCAGACTGACCAACCACTT 23
 Db 149 ACCACGACTGAGCACGCCATT 127
 RESULT 2
 AF086548/C
 LOCUS AF086548
 DEFINITION Heterosigma akashiwo large subunit ribosomal RNA gene, partial
 Sequence.
 ACCESSION AF086548
 VERSION AF086548.1 GI:3695263
 KEYWORDS Heterosigma akashiwo.
 SOURCE
 ORGANISM Heterosigma akashiwo.
 REFERENCE
 1 (bases 1 to 713)
 AUTHORS Connell,L.
 TITLE Direct Submission
 JOURNAL Submitted (26-AUG-1998) Environmental Conservation Division,
 National Marine Fisheries Service, 2725 Montalke Blvd East,
 Seattle, WA 98112, USA
 FEATURES source
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 /organism="Heterosigma akashiwo"
 /strain="CCMP-422"
 /db_xref="taxon:2829"
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 /note="Contains variable domains D1-D3"
 /product="large subunit ribosomal RNA"
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 Best Local Similarity 100.0%; Pred. No. 0.15; Matches 23;
 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Features 3 (bases 1 to 715)
 REFERENCE
 2 (bases 1 to 715)
 AUTHORS Tyrrell,J.V., Scholin,C.A., Bergquist,P.R. and Bergquist,P.L.
 TITLE Phylogeny and Enumeration of Heterosigma akashiwo and Fibrocapsa
 Japonica (Raphidophyceae) Using rRNA-targeted Oligonucleotides
 JOURNAL Unpublished
 REFERENCE
 3 (bases 1 to 715)
 AUTHORS Tyrrell,J.V., Bergquist,P.R., Mackenzie,L. and Bergquist,P.L.
 TITLE Direct Submission
 JOURNAL Submitted (03-DEC-1999) Research and Development, Monterey Bay
 Aquarium Research Institute, 7700 Sandholdt Road, Moss Landing, CA
 95039-0628, USA
 FEATURES source
 1. .715
 /organism="Heterosigma sp. CAWR10"
 /strain="CAWR10"
 /db_xref="taxon:147349"
 /note="similar to Heterosigma akashiwo sequence AF210741"
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 /note="D1 and D2 domains; similar to Heterosigma akashiwo
 sequence presented in GenBank Accession Number AF210741"
 BASE COUNT 166 a 148 c 212 g 189 t
 ORIGIN Query Match 100.0%; Score 23; DB 8; Length 715;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Features 3 (bases 1 to 715)
 REFERENCE
 2 (bases 1 to 715)
 AUTHORS Tyrrell,J.V., Bergquist,P.R., MacKenzie,L. and Bergquist,P.L.
 TITLE Phlogeny of the Raphidophytes Based on Large-subunit rRNA Gene
 JOURNAL Unpublished
 REFERENCE
 3 (bases 1 to 715)
 AUTHORS Tyrrell,J.V., Bergquist,P.R., MacKenzie,L. and Bergquist,P.L.
 TITLE Direct Submission
 JOURNAL Submitted (03-DEC-1999) Research and Development, Monterey Bay
 Aquarium Research Institute, 7700 Sandholdt Road, Moss Landing, CA
 95039-0628, USA
 FEATURES source
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 /organism="Heterosigma sp. CAWR10"
 /strain="CAWR10"
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 sequence presented in GenBank Accession Number AF210741"
 BASE COUNT 166 a 148 c 212 g 189 t
 ORIGIN Query Match 100.0%; Score 23; DB 8; Length 715;
 Best Local Similarity 100.0%; Pred. No. 0.15;
 Features 3 (bases 1 to 715)

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 17, 2002, 08:07:35 ; Search time 978.267 Seconds
(without alignments)
492.003 Million cell updates/sec

Title: US-09-780-113D-15

Perfect score: 23
Sequence: 1 accatcgactggacgacattt 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_cv:*

6: gb_pat:*

7: gb_ph:*

8: gb_pr1:*

9: gb_pr:*

10: gb_ro:*

11: gb_srs:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_srs:*

28: em_un:*

29: em_vl:*

30: em_htg,hum:*

31: em_htg,inv:*

32: em_htg_other:*

33: em_htg_inv:*

ALIGNMENTS

RESULT 1
AF042820/C
LOCUS AF042820
DEFINITION Heterosigma akashiwo 24S large subunit ribosomal RNA partial sequence.
ACCESSION AF042820
VERSION AF042820.1 GI:2827390
KEYWORDS
ORGANISM Heterosigma akashiwo.
REFERENCE I (bases 1 to 712)
AUTHORS Lee, S.W., Park, C.G. and Park, Y.S.
TITLE 24S ribosomal RNA sequence analysis of dinoflagellates isolated from redtide in southern coast of Korea
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 712)
AUTHORS Lee, S.W., Park, C.G. and Park, Y.S.
TITLE Direct Submission
JOURNAL Submitted (14-JAN-1998) Department of Microbiology, Inje University, Obangdong 607, Kimhae 621-749, Korea
FEATURES Location/Qualifiers
Source 1. .712

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
8				